

RAW SEQUENCE LISTING

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Application Serial Number: 09/591,632-D
Source: IFW16
Date Processed by STIC: 03/27/2006

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IFW16

RAW SEQUENCE LISTING

DATE: 03/27/2006

PATENT APPLICATION: US/09/591,632D

TIME: 09:53:48

Input Set : A:\34978a.txt

Output Set: N:\CRF4\03272006\I591632D.raw

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3 <110> APPLICANT: Lindquist, et al.
5 <120> TITLE OF INVENTION: RECOMBINANT PRION-LIKE GENES AND PROTEINS
6   AND MATERIALS AND METHODS COMPRISING SAME
8 <130> FILE REFERENCE: 30554/34978A
10 <140> CURRENT APPLICATION NUMBER: US 09/591,632D
11 <141> CURRENT FILING DATE: 2000-06-09
13 <150> PRIOR APPLICATION NUMBER: US 60/138,833
14 <151> PRIOR FILING DATE: 1999-06-09
16 <160> NUMBER OF SEQ ID NOS: 70
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 3321
22 <212> TYPE: DNA
23 <213> ORGANISM: Saccharomyces cerevisiae
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (739)..(2796)
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35 attggagttt gaagaaaatc ccaaccctac ggtagaaaat tgaatatcgt atctgtttat      180
37 acacacatac atacatttat atttataata agcggttaaaa tttcggcaga atatctgtca      240
39 accacacaaa aatcatacaa cgaatggtat atgcttcatt tctttgtttc gcattagctg      300
41 cgctatttga ctcaaattat tattttttac taagacgacg cgtcacagtg ttcgagctcg      360
43 tgtcatttct ttgtaatctt tcttaaacca cttcataaag ttgtgaagtt catagcaaaa      420
45 ttcttccgca aaaagatgaa tcttagttct cagcccacca aaagaggtac atgctaagat      480
47 catacagaag ttattgtcac ttcttacctt gctcttaaat gtacattaca accgggtatt      540
49 atatcttaca tcatcgataa atatgatctt tctttatgga gaaaattttt ttttcaactcg      600
51 accaaaagctc ccattgcttc tgaagagtgt agtgtatatt ggtacatctt ctcttgaaag      660
53 actccattgt actgtaacaa aaagcgggtt cttcatcgac ttgctcggaa taacatctat      720
55 atctgcccac tagcaaca atg tcg gat tca aac caa ggc aac aat cag caa      771
56                               Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln
57                               1           5           10
59 aac tac cag caa tac agc cag aac ggt aac caa caa caa ggt aac aac      819
60 Asn Tyr Gln Gln Tyr Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn
61                               15           20           25
63 aga tac caa ggt tat caa gct tac aat gct caa gcc caa cct gca ggt      867
64 Arg Tyr Gln Gly Tyr Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly
65                               30           35           40
67 ggg tac tac caa aat tac caa ggt tat tct ggg tac caa caa ggt ggc      915
68 Gly Tyr Tyr Gln Asn Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly
69                               45           50           55
71 tat caa cag tac aat ccc gac gcc ggt tac cag caa cag tat aat cct      963

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75	caa	gga	ggc	tat	caa	cag	tac	aat	cct	caa	ggc	ggt	tat	cag	cag	caa	1011
76	Gln	Gly	Gly	Tyr	Gln	Gln	Tyr	Asn	Pro	Gln	Gly	Gly	Tyr	Gln	Gln	Gln	
77					80					85					90		
79	ttc	aat	cca	caa	ggt	ggc	cgt	gga	aat	tac	aaa	aac	ttc	aac	tac	aat	1059
80	Phe	Asn	Pro	Gln	Gly	Gly	Arg	Gly	Asn	Tyr	Lys	Asn	Phe	Asn	Tyr	Asn	
81				95					100					105			
83	aac	aat	ttg	caa	gga	tat	caa	gct	ggt	ttc	caa	cca	cag	tct	caa	ggt	1107
84	Asn	Asn	Leu	Gln	Gly	Tyr	Gln	Ala	Gly	Phe	Gln	Pro	Gln	Ser	Gln	Gly	
85			110					115					120				
87	atg	tct	ttg	aac	gac	ttt	caa	aag	caa	caa	aag	cag	gcc	gct	ccc	aaa	1155
88	Met	Ser	Leu	Asn	Asp	Phe	Gln	Lys	Gln	Gln	Lys	Gln	Ala	Ala	Pro	Lys	
89			125					130					135				
91	cca	aag	aag	act	ttg	aag	ctt	gtc	tcc	agt	tcc	ggt	atc	aag	ttg	gcc	1203
92	Pro	Lys	Lys	Thr	Leu	Lys	Leu	Val	Ser	Ser	Ser	Gly	Ile	Lys	Leu	Ala	
93	140					145					150					155	
95	aat	gct	acc	aag	aag	gtt	ggc	aca	aaa	cct	gcc	gaa	tct	gat	aag	aaa	1251
96	Asn	Ala	Thr	Lys	Lys	Val	Gly	Thr	Lys	Pro	Ala	Glu	Ser	Asp	Lys	Lys	
97				160						165				170			
99	gag	gaa	gag	aag	tct	gct	gaa	acc	aaa	gaa	cca	act	aaa	gag	cca	aca	1299
100	Glu	Glu	Glu	Lys	Ser	Ala	Glu	Thr	Lys	Glu	Pro	Thr	Lys	Glu	Pro	Thr	
101				175						180				185			
103	aag	gtc	gaa	gaa	cca	gtt	aaa	aag	gag	gag	aaa	cca	gtc	cag	act	gaa	1347
104	Lys	Val	Glu	Glu	Pro	Val	Lys	Lys	Glu	Glu	Lys	Pro	Val	Gln	Thr	Glu	
105			190						195					200			
107	gaa	aag	acg	gag	gaa	aaa	tcg	gaa	ctt	cca	aag	gta	gaa	gac	ctt	aaa	1395
108	Glu	Lys	Thr	Glu	Glu	Lys	Ser	Glu	Leu	Pro	Lys	Val	Glu	Asp	Leu	Lys	
109		205					210					215					
111	atc	tct	gaa	tca	aca	cat	aat	acc	aac	aat	gcc	aat	gtt	acc	agt	gct	1443
112	Ile	Ser	Glu	Ser	Thr	His	Asn	Thr	Asn	Asn	Ala	Asn	Val	Thr	Ser	Ala	
113	220					225					230				235		
115	gat	gcc	ttg	atc	aag	gaa	cag	gaa	gaa	gaa	gtg	gat	gac	gaa	gtt	gtt	1491
116	Asp	Ala	Leu	Ile	Lys	Glu	Gln	Glu	Glu	Glu	Val	Asp	Asp	Glu	Val	Val	
117				240						245				250			
119	aac	gat	atg	ttt	ggt	ggt	aaa	gat	cac	gtt	tct	tta	att	ttc	atg	ggt	1539
120	Asn	Asp	Met	Phe	Gly	Gly	Lys	Asp	His	Val	Ser	Leu	Ile	Phe	Met	Gly	
121			255						260					265			
123	cat	gtt	gat	gcc	ggt	aaa	tct	act	atg	ggt	ggt	aat	cta	cta	tac	ttg	1587
124	His	Val	Asp	Ala	Gly	Lys	Ser	Thr	Met	Gly	Gly	Asn	Leu	Leu	Tyr	Leu	
125			270						275					280			
127	act	ggc	tct	gtg	gat	aag	aga	act	att	gag	aaa	tat	gaa	aga	gaa	gcc	1635
128	Thr	Gly	Ser	Val	Asp	Lys	Arg	Thr	Ile	Glu	Lys	Tyr	Glu	Arg	Glu	Ala	
129		285					290					295					
131	aag	gat	gca	ggc	aga	caa	ggt	tgg	tac	ttg	tca	tgg	gtc	atg	gat	acc	1683
132	Lys	Asp	Ala	Gly	Arg	Gln	Gly	Trp	Tyr	Leu	Ser	Trp	Val	Met	Asp	Thr	
133	300					305					310				315		
135	aac	aaa	gaa	gaa	aga	aat	gat	ggt	aag	act	atc	gaa	gtt	ggt	aag	gcc	1731
136	Asn	Lys	Glu	Glu	Arg	Asn	Asp	Gly	Lys	Thr	Ile	Glu	Val	Gly	Lys	Ala	

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137		320		325		330	
139	tac ttt gaa act gaa aaa agg cgt tat acc ata ttg gat gct cct ggt						1779
140	Tyr Phe Glu Thr Glu Lys Arg Arg Tyr Thr Ile Leu Asp Ala Pro Gly						
141		335		340		345	
143	cat aaa atg tac gtt tcc gag atg atc ggt ggt gct tct caa gct gat						1827
144	His Lys Met Tyr Val Ser Glu Met Ile Gly Gly Ala Ser Gln Ala Asp						
145		350		355		360	
147	gtt ggt gtt ttg gtc att tcc gcc aga aag ggt gag tac gaa acc ggt						1875
148	Val Gly Val Leu Val Ile Ser Ala Arg Lys Gly Glu Tyr Glu Thr Gly						
149		365		370		375	
151	ttt gag aga ggt ggt caa act cgt gaa cac gcc cta ttg gcc aag acc						1923
152	Phe Glu Arg Gly Gly Gln Thr Arg Glu His Ala Leu Leu Ala Lys Thr						
153	380		385		390		395
155	caa ggt gtt aat aag atg gtt gtc gtc gta aat aag atg gat gac cca						1971
156	Gln Gly Val Asn Lys Met Val Val Val Asn Lys Met Asp Asp Pro						
157		400		405		410	
159	acc gtt aac tgg tct aag gaa cgt tac gac caa tgt gtg agt aat gtc						2019
160	Thr Val Asn Trp Ser Lys Glu Arg Tyr Asp Gln Cys Val Ser Asn Val						
161		415		420		425	
163	agc aat ttc ttg aga gca att ggt tac aac att aag aca gac gtt gta						2067
164	Ser Asn Phe Leu Arg Ala Ile Gly Tyr Asn Ile Lys Thr Asp Val Val						
165		430		435		440	
167	ttt atg cca gta tcc ggc tac agt ggt gca aat ttg aaa gat cac gta						2115
168	Phe Met Pro Val Ser Gly Tyr Ser Gly Ala Asn Leu Lys Asp His Val						
169		445		450		455	
171	gat cca aaa gaa tgc cca tgg tac acc ggc cca act ctg tta gaa tat						2163
172	Asp Pro Lys Glu Cys Pro Trp Tyr Thr Gly Pro Thr Leu Leu Glu Tyr						
173	460		465		470		475
175	ctg gat aca atg aac cac gtc gac cgt cac atc aat gct cca ttc atg						2211
176	Leu Asp Thr Met Asn His Val Asp Arg His Ile Asn Ala Pro Phe Met						
177		480		485		490	
179	ttg cct att gcc gct aag atg aag gat cta ggt acc atc gtt gaa ggt						2259
180	Leu Pro Ile Ala Ala Lys Met Lys Asp Leu Gly Thr Ile Val Glu Gly						
181		495		500		505	
183	aaa att gaa tcc ggt cat atc aaa aag ggt caa tcc acc cta ctg atg						2307
184	Lys Ile Glu Ser Gly His Ile Lys Lys Gly Gln Ser Thr Leu Leu Met						
185		510		515		520	
187	cct aac aaa acc gct gtg gaa att caa aat att tac aac gaa act gaa						2355
188	Pro Asn Lys Thr Ala Val Glu Ile Gln Asn Ile Tyr Asn Glu Thr Glu						
189		525		530		535	
191	aat gaa gtt gat atg gct atg tgt ggt gag caa gtt aaa cta aga atc						2403
192	Asn Glu Val Asp Met Ala Met Cys Gly Glu Gln Val Lys Leu Arg Ile						
193	540		545		550		555
195	aaa ggt gtt gaa gaa gaa gac att tca cca ggt ttt gta cta aca tcg						2451
196	Lys Gly Val Glu Glu Glu Asp Ile Ser Pro Gly Phe Val Leu Thr Ser						
197		560		565		570	
199	cca aag aac cct atc aag agt gtt acc aag ttt gta gct caa att gct						2499
200	Pro Lys Asn Pro Ile Lys Ser Val Thr Lys Phe Val Ala Gln Ile Ala						
201		575		580		585	

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204 Ile Val Glu Leu Lys Ser Ile Ile Ala Ala Gly Phe Ser Cys Val Met
205          590                      595                      600
207 cat gtt cat aca gca att gaa gag gta cat att gtt aag tta ttg cac      2595
208 His Val His Thr Ala Ile Glu Glu Val His Ile Val Lys Leu Leu His
209          605                      610                      615
211 aaa tta gaa aag ggt acc aac cgt aag tca aag aaa cca cct gct ttt      2643
212 Lys Leu Glu Lys Gly Thr Asn Arg Lys Ser Lys Lys Pro Pro Ala Phe
213 620                      625                      630                      635
215 gct aag aag ggt atg aag gtc atc gct gtt tta gaa act gaa gct cca      2691
216 Ala Lys Lys Gly Met Lys Val Ile Ala Val Leu Glu Thr Glu Ala Pro
217          640                      645                      650
219 gtt tgt gtg gaa act tac caa gat tac cct caa tta ggt aga ttc act      2739
220 Val Cys Val Glu Thr Tyr Gln Asp Tyr Pro Gln Leu Gly Arg Phe Thr
221          655                      660                      665
223 ttg aga gat caa ggt acc aca ata gca att ggt aaa att gtt aaa att      2787
224 Leu Arg Asp Gln Gly Thr Thr Ile Ala Ile Gly Lys Ile Val Lys Ile
225          670                      675                      680
227 gcc gag taa atttcttgca aacataagta aatgcaaaca caataatacc      2836
228 Ala Glu
229          685
231 gatcataaag cattttcttc tatattaaaa aacaagggtt aataaagctg ttatatatat      2896
233 atatatatat atagacgtat aattagttta gttctttttg taccatatac cataaacaag      2956
235 gtaaaacttca cctctcaata tatctagaat ttcataaaaa tatctagcaa ggtttcaact      3016
237 ccttcaatca cgttttcatc ataacccttc cccggcggtta tttcagaatg tgcaaaatct      3076
239 attagtgaca tggaactcaa agaaccagtt gtttttttgt cctttgggtcc ttcgctgctt      3136
241 ccctcggcat catcatcatc atcatcatca ttatcatcat cgtcgtcatc atcgtctata      3196
243 aaatcatctc gcataagttt gtcaacatca tttagtaatt cccatcgctc cgggtctcct      3256
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262          20          25          30
265 Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
266          35          40          45
269 Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
270          50          55          60
273 Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln
274 65          70          75          80
277 Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Phe Asn Pro Gln Gly
278          85          90          95
281 Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly
282          100          105          110

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285 Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu Asn Asp
286      115      120      125
289 Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu
290      130      135      140
293 Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys
294 145      150      155      160
297 Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser
298      165      170      175
301 Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu Glu Pro
302      180      185      190
305 Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr Glu Glu
306      195      200      205
309 Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu Ser Thr
310      210      215      220
313 His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu Ile Lys
314 225      230      235      240
317 Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp Met Phe Gly
318      245      250      255
321 Gly Lys Asp His Val Ser Leu Ile Phe Met Gly His Val Asp Ala Gly
322      260      265      270
325 Lys Ser Thr Met Gly Gly Asn Leu Leu Tyr Leu Thr Gly Ser Val Asp
326      275      280      285
329 Lys Arg Thr Ile Glu Lys Tyr Glu Arg Glu Ala Lys Asp Ala Gly Arg
330      290      295      300
333 Gln Gly Trp Tyr Leu Ser Trp Val Met Asp Thr Asn Lys Glu Glu Arg
334 305      310      315      320
337 Asn Asp Gly Lys Thr Ile Glu Val Gly Lys Ala Tyr Phe Glu Thr Glu
338      325      330      335
341 Lys Arg Arg Tyr Thr Ile Leu Asp Ala Pro Gly His Lys Met Tyr Val
342      340      345      350
345 Ser Glu Met Ile Gly Gly Ala Ser Gln Ala Asp Val Gly Val Leu Val
346      355      360      365
349 Ile Ser Ala Arg Lys Gly Glu Tyr Glu Thr Gly Phe Glu Arg Gly Gly
350      370      375      380
353 Gln Thr Arg Glu His Ala Leu Leu Ala Lys Thr Gln Gly Val Asn Lys
354 385      390      395      400
357 Met Val Val Val Val Asn Lys Met Asp Asp Pro Thr Val Asn Trp Ser
358      405      410      415
361 Lys Glu Arg Tyr Asp Gln Cys Val Ser Asn Val Ser Asn Phe Leu Arg
362      420      425      430
365 Ala Ile Gly Tyr Asn Ile Lys Thr Asp Val Val Phe Met Pro Val Ser
366      435      440      445
369 Gly Tyr Ser Gly Ala Asn Leu Lys Asp His Val Asp Pro Lys Glu Cys
370      450      455      460
373 Pro Trp Tyr Thr Gly Pro Thr Leu Leu Glu Tyr Leu Asp Thr Met Asn
374 465      470      475      480
377 His Val Asp Arg His Ile Asn Ala Pro Phe Met Leu Pro Ile Ala Ala
378      485      490      495
381 Lys Met Lys Asp Leu Gly Thr Ile Val Glu Gly Lys Ile Glu Ser Gly

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